





RAW SEQUENCE LISTING PATENT APPLICATION US/09/080,140

DATE: 05/29/98 TIME: 08:26:59

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This Raw Listing contains the General Information Section and up to the first 5 pages.

	1	SEQUENCE LISTING
	2 3 (1)	General Information
	4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9	(i) APPLICANT: BILLING-MEDEL, PATRICIA COHEN, MAURICE COLPITTS, TRACEY L. FRIEDMAN, PAULA N. GORDON, JULIAN GRANADOS, EDWARD N. HODGES, STEVEN C. KLASS, MICHAEL R. KRATOCHVIL, JON D. ROBERTS-RAPP, LISA RUSSELL, JOHN C. STROUPE, STEPHEN D.
	9 9 10 11 12 23 24 25 26 27 28 28 29 30 31 32 33 34 35 36 37 38 38 39 30 30 30 30 30 30 30 30 30 30 30 30 30	(ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF THE PROSTATE (iii) NUMBER OF SEQUENCES: 31 (iv) CORRESPONDENCE ADDRESS: (A) ADDRESSEE: Abbott Laboratories (B) STREET: 100 Abbott Park Road (C) CITY: Abbott Park (D) STATE: IL (E) COUNTRY: USA (F) ZIP: 60064-3500 (v) COMPUTER READABLE FORM: (A) MEDIUM TYPE: Diskette (B) COMPUTER: IBM Compatible (C) OPERATING SYSTEM: DOS (D) SOFTWARE: FastSEQ for Windows Version 2.0 (vi) CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: (B) FILING DATE: (C) CLASSIFICATION:
4	:4 :5 :6	(vii) PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: 08/856,653

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	11,1 01 011 010 1010
47	(B) FILING DATE: 15-MAY-1997
48	
49	
50	
51	(viii) ATTORNEY/AGENT INFORMATION:
52	(A) NAME: Becker, Cheryl L.
53	(B) REGISTRATION NUMBER: 35,441
54	(C) REFERENCE/DOCKET NUMBER: 6105.US.P1
55	
56	(ix) TELECOMMUNICATION INFORMATION:
57	(A) TELEPHONE: 847/935-1729
58	(B) TELEFAX: 847/938-2623
59	(C) TELEX:
60	(2) INFORMATION FOR SEQ ID NO:1:
61	
62	(i) SEQUENCE CHARACTERISTICS:
63	(A) LENGTH: 290 base pairs
64	(B) TYPE: nucleic acid
65	(C) STRANDEDNESS: single
66	(D) TOPOLOGY: linear
67	, ,
68	(ix) FEATURE:
69	(A) NAME/KEY: base_polymorphism
70	(B) LOCATION: 31
71	(D) OTHER INFORMATION: /note= " N' represents an A or G or
72	T or C polymorphism at this position"
73	
74	(ix) FEATURE:
75	(A) NAME/KEY: base polymorphism
76	(B) LOCATION: 232
77	(D) OTHER INFORMATION: /note= " N' represents an A or G or
78	T or C polymorphism at this position"
79	
80	(ix) FEATURE:
81	(A) NAME/KEY: base polymorphism
82	(B) LOCATION: 275
83	(D) OTHER INFORMATION: /note= " N' represents an A or G or
84	T or C polymorphism at this position"
85	
86	(ix) FEATURE:
87	(A) NAME/KEY: base_polymorphism
88	(B) LOCATION: 284
89	(D) OTHER INFORMATION: /note= " N' represents an A or G or
90	T or C polymorphism at this position"
91	
92	
93	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
94	
95	CATTTGAGGC CATATAAAGT CACCTGAGGC NCTCTCCACC ACAGCCCACC AGTGACCATG 60
96	AAGGCTGTGC TGCTTGCCCT GTTGATGGCA GGCTTGGCCC TGCAGCCAGG CACTGCCCTG 120
97	CTGTGCTACT CCTGCAAAGC CCAGGTGAGC AACGAGGACT GCCTGCAGGT GGAGAACTGC 180
98	ACCCAGCTGG GGGAGCAGTG CTGGACCGCG CGCATCCGCG CAGTTGGCCT CNTGACCGTC 240
99	ATCAGCAAAG CTGCAGCTTG AACTGCGTGG ATGANTCACA GGANTACTAC 290

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	100		
	101	(2) INFORMATION FOR SEQ ID NO:2:	
	102		
	103	(i) SEQUENCE CHARACTERISTICS:	
	104	(A) LENGTH: 293 base pairs	
	105	(B) TYPE: nucleic acid	
	106	(C) STRANDEDNESS: single	
	107	(D) TOPOLOGY: linear	
	108		
	109		
	110	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
	111		
	112	GAGGCCCTCT CCACCACAGC CCACCAGTGA CCATGAAGGC TGTGCTGCTT GCCCTGTTGA	, 60
	113	TGGCAGGCTT GGCCCTGCAG CCAGGCACTG CCCTGCTGTG CTACTCCTGC AAAGCCCAGG	120
	114	TGAGCAACGA GGACTGCCTG CAGGTGGAGA ACTGCACCCA GCTGGGGGAG CAGTGCTGGA	180
	115	CCGCGCGCAT CCGCGCAGTT GGCCTCCTGA CCGTCATCAG CAAAGGCTGC AGCTTGAACT	240
	116	GCGTGGATGA CTCACAGGAC TACTACGTGG GCAAGAAGAA CATCACGTGC TGT	293
~	117		
	118	(2) INFORMATION FOR SEQ ID NO:3:	
<u>.</u>	119		
<u>L</u>	120	(i) SEQUENCE CHARACTERISTICS:	
Q.	121	(A) LENGTH: 279 base pairs	
	122	(B) TYPE: nucleic acid	
브	123	(C) STRANDEDNESS: single	
	124	(D) TOPOLOGY: linear	
	125 126		
	126	(mi) GROUPIOE DECORTOMION. GEO ID NO. 2.	
	127	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
i	128	CAGTGACCAT GAAGGCTGTG CTGCTTGCCC TGTTGATGGC AGGCTTGGCC CTGCAGCCAG	60
FI.	130	GCACTGCCCT GCTGTGCTAC TCCTGCAAAG CCCAGGTGAG CAACGAGGAC TGCCTGCAGG	120
÷	131	TGGAGAACTG CACCCAGCTG GGGGAGCAGT GCTGGACCGC GCGCATCCGC GCAGTTGGCC	180
f	132	TCCTGACCGT CATCAGCAAA GGCTGCAGCT TGAACTGCGT GGATGACTCA CAGGACTACT	240
Ō	133	ACGTGGGCAA GAAGAACATC ACGTGCTGTG ACACCGACT	279
- Ti	134		
	135	(2) INFORMATION FOR SEQ ID NO:4:	
	136	(=, ===================================	
	137	(i) SEQUENCE CHARACTERISTICS:	
	138	(A) LENGTH: 207 base pairs	
	139	(B) TYPE: nucleic acid	
	140	(C) STRANDEDNESS: single	
	141	(D) TOPOLOGY: linear	
	142		
	143		
	144	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
	145		
	146	GTGACCATGA AGGCTGTGCT GCTTGCCCTG TTGATGGCAG GCTTGGCCCT GCAGCCAGGC	60
	147	ACTGCCCTGC TGTGCTACTC CTGCAAAGCC CAGGTGAGCA ACGAGGACTG CCTGCAGGTG	120
	148	GAGAACTGCA CCCAGCTGGG GGAGCAGTGC TGGACCGCGC GCATCCGCGC AGTTGGCCTC	180
	149	CTGACCGTCA TCAGCAAAGG CTGCAGC	207
	150		
	151	(2) INFORMATION FOR SEQ ID NO:5:	

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	153	(i) SEQUENCE CHARACTERISTICS:	
	154	(A) LENGTH: 265 base pairs	
	155	(B) TYPE: nucleic acid	
	156	(C) STRANDEDNESS: single	
	157	(D) TOPOLOGY: linear	
		(b) lorologi: linear	
	158		
	159		
	160	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
	161		
	162	CGAGGACTGC CTGCAGGTGG AGAACTGCAC CCAGCTGGGG GAGCAGTGCT GGACCGCGCG	60
	163	***************************************	120
	164	•••••	180
	165		240
	166	ACTCGGCCTG CTGCTCTGGG GACCC	265
	167		
	168	(2) INFORMATION FOR SEQ ID NO:6:	
	169	· •	
	170	(i) SEQUENCE CHARACTERISTICS:	
	171	(A) LENGTH: 230 base pairs	
	172	(B) TYPE: nucleic acid	
	173	(C) STRANDEDNESS: single	
	174	(D) TOPOLOGY: linear	
IJ	175	(b) Torologi. Illegi	
	175		
		(wi) GROUPINGE DECORPORATION, GRO ID NO.6.	
<u></u>	177	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
-	178	amagmana a sagaraman garrang agarang agagagan agagmana agagmana	60
	179	GTGCTGTGAC ACCGACTTGT GCAACGCCAG CGGGGCCCAT GCCCTGCAGC CGGCTGCCGC	60
:	180	***************************************	120
3	181		180
n	182	TCACAGACCT GGCCCAGTGG GAGCCTGTCC TGGTTCCTGA GGCACATCCT	230
	183		
	184	(2) INFORMATION FOR SEQ ID NO:7:	
<i>]</i>	185		
n D	186	(i) SEQUENCE CHARACTERISTICS:	
Ħ	187	(A) LENGTH: 233 base pairs	
	188	(B) TYPE: nucleic acid	
	189	(C) STRANDEDNESS: single	
	190	(D) TOPOLOGY: linear	
	191		
	192	(ix) FEATURE:	
	193	(A) NAME/KEY: base polymorphism	
	194	(B) LOCATION: 70	
	195	(D) OTHER INFORMATION: /note= " N' represents an A or G o	r
	196	T or C polymorphism at this position"	
	197	Total portional and and portion	
	198		
	199	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
	200	(VI) PEROPUCE DEPONTATION. PER ID HO. 1.	
		C C C C C C C C C C	60
	201	CTGGCCCAGT GGGAGCCTGT CCTGGTTCCT GAGGCACATC CTAACGCAAG TCTGACCATG	120
	202		
	203		180
	204	TGCTGTTTCC ATGGCCCAGC ATTCTCCACC CTTAACCCTG TGCTCAGGCA CCT	233
	205		

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	206	(2) INFORMATION FOR SEQ ID NO:8:
	207	
	208	(i) SEQUENCE CHARACTERISTICS:
	209	(A) LENGTH: 250 base pairs
	210	(B) TYPE: nucleic acid
	211	(C) STRANDEDNESS: single
	212	(D) TOPOLOGY: linear
	213	. ,
	214	(ix) FEATURE:
	215	(A) NAME/KEY: base polymorphism
	216	(B) LOCATION: 60
	217	(D) OTHER INFORMATION: /note= " N' represents an A or G or
	218	T or C polymorphism at this position"
	219	Tot e polymorphism de this position
	220	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
	220	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:0:
	221	CONCENTRAL CONTRACTOR DESCRIPTION AND ADMINISTRAL CARROLLERY (A)
		GTCCTGGTTC CTGAGGCACA TCCTAACGCA AGTCTGACCA TGTATGTCTG CACCCCTGTN 60
==	223	CCCCACCTG ACCCTCCCAT GGCCCTCTCC AGGACTCCCA CCCGGCAGAT CAGCTCTAGT 120
닐	224	GACACAGATC CGCCTGCAGA TGGCCCCTCC AACCCTCTCT GCTGCTGTTT CCATGGCCCA 180
₩.	225	GCATTCTCCA CCCTTAACCC TGTGCTCAGG CACCTCTTCC CCCAGGAAGC CTTCCCTGCC 240
	226	CACCCCATCT 250
Ħ	227	
	228	(2) INFORMATION FOR SEQ ID NO:9:
	229	
=	230	(i) SEQUENCE CHARACTERISTICS:
=	231	(A) LENGTH: 259 base pairs
=	232	(B) TYPE: nucleic acid
	233	(C) STRANDEDNESS: single
=	234	(D) TOPOLOGY: linear
=	235	
<i>§</i> }	236	
	237	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
Π	238	
Ō	239	TAACCCTGTG CTCAGGCACC TCTTCCCCCA GGAAGCCTTC CCTGCCCACC CCATCTATGA 60
T	240	CTTGAGCCAG GTCTGGTCCG TGGTGTCCCC CGCACCCAGC AGGGGACAGG CACTCAGGAG 120
-	241	GGCCCAGTAA AGGCTGAGAT GAAGTGGACT GAGTAGAACT GGAGGACAAG AGTCGACGTG 180
	242	AGTTCCTGGG AGTCTCCAGA GATGGGGCCT GGAGGCCTGG AGGAAGGGGC CAGGCCTCAC 240
	243	ATTCGTGGGG CTCCCTGAA 259
	244	
	245	(2) INFORMATION FOR SEQ ID NO:10:
	246	· ·
	247	(i) SEQUENCE CHARACTERISTICS:
	248	(A) LENGTH: 253 base pairs
	249	(B) TYPE: nucleic acid
	250	(C) STRANDEDNESS: single
	251	(D) TOPOLOGY: linear
	252	/2/ 10102011 22:1001
	253	
	254	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
	254	(VI) DESORTEITON: DES IN MO:IA:
	256	ATCTATGACT TGAGCCAGGT CTGGTCCGTG GTGTCCCCCG CACCCAGCAG GGGACAGGCA 60
	256	CTCAGGAGGG CCCAGTAAAG GCTGAGATGA AGTGGACTGA GTAGAACTGG AGGACAAGAG 120
	257	TCAGGAGGG CCCAGTAAAG GCTGAGATGA AGTGGACTGA GTAGAACTGG AGGACAAGAG 120 TCCAGCTGAG TTTCCTCCCAG TCTCCAGACA TCCCCCCCCA 180

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/09/080,140

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Original Text

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Response Exceeds Line Limitations

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STROUPE, STEPHEN D.

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